LISTING OF CLAIMS

Claims 1-51 (Cancelled)

Claim 52 (Currently Amended) A method for determining coding features within a nucleic acid sequence by determining a probability for each of one or more states for more than one examined nucleotide in said nucleic acid sequence, comprising:

a) determining an initial oligonucleotide probability for each of said states for an initial oligonucleotide in a window of a first examined nucleotide;

b) determining transition probabilities for each of said states for nucleotides within said window following said initial oligonucleotide;

c) using said initial oligonucleotide probability and said transition probabilities to determine a plurality of window probabilities, wherein said plurality comprises a window probability corresponding to each of said states for said examined nucleotide;

d) applying a bias function to said plurality of window probabilities, to determine a probability for each of said states for said examined nucleotide, wherein a value being used in said bias function is different in at least one state from the other states for said examined nucleotide;

e) repeating steps a) through d) for each remaining examined nucleotide in said nucleic acid sequence,

wherein said more than one examined nucleotide are contiguous, and step e) is performed sequentially from said first examined nucleotide to a last examined nucleotide,

wherein said probability for each of said states for said more than one examined nucleotide is determined using an inhomogeneous Markov model having eight states, wherein said eight states are: first reading frame positive strand (1+); second reading frame positive strand (2+); third reading frame positive strand (3+); first reading frame negative strand (1-); second reading frame negative strand (2-); third reading frame negative strand (3-); noncoding positive strand (N+); and noncoding negative strand (N-),

wherein said probability for each of said states for said more than one examined nucleotide is determined using the equation

$$P'(\sigma \mid S) = \frac{\phi(\sigma) \cdot P(\sigma) \cdot P(S \mid \sigma)}{\sum_i [\phi(i) \cdot P(i) \cdot P(S \mid i)]},$$

wherein i is an element in said eight states,

wherein σ is an element in said eight states,

wherein $P'(\sigma \mid S)$ is said probability for said (σ) for said nucleic acid sequence (S),

wherein $P(S \mid \sigma)$ is said probability for said nucleic acid sequence (S) while in said (σ),

wherein $P(S \mid i)$ is said probability for said nucleic acid sequence (S) corresponding to (i),

wherein $P(i)$ is a probability for (i) among said eight states,

wherein $P(\sigma)$ is a probability for (σ) among said eight states,

wherein $\phi(\sigma)$ is said bias function corresponding to said state (σ),

wherein $\phi(i)$ is said bias function corresponding to said state ([[I]]*i*),

f) ~~providing~~ outputting said nucleic acid sequence as most probable states of said probability states for each of said states for each of more than one examined nucleotide wherein said most probable states demarcate said coding features of said nucleic acid sequence and ~~providing~~ outputting said coding features as a translated protein sequence.

Claims 53-55 (Cancelled)

Claim 56 (Previously presented) The method of claim 52, wherein said nucleic acid sequence is part of a longer nucleic acid sequence.

Claim 57 (Previously presented) The method of claim 52, wherein said examined nucleotide in said more than one examined nucleotide is the middle nucleotide in its own window.

Claims 58-59 (Cancelled)

Claim 60 (Previously presented) The method of claim 52, wherein the value being used in said bias function is between 0.0 and 0.9, or greater than 1.1, in one or more of said states for said nucleotide.